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logo
NTDB id 124 BSU 16930 NP 389575.2              MEFPKKAEIIAVGSELLLGQIANTNAQFISKQLAEIGVNVFYHTAVGDNPERLKQVIRIAEERSDFIIFSGGLGPTKDDL   80
NTDB id 462 GPW51 RS00385 WP 012774894.1       ....MKAELIAVGTEILTGQIINTNAQFLSEKCAELGIDVYFHTAVGDNEGRLLSTLEVASKRSNMVVLCGGLGPTEDDL   76
NTDB id 412 SMU RS09535 WP 002262393.1         ....MKSEIIAVGTEILTGQIVNTNSQFLSEKFAELGIDVYFQTAVGDNEERLLSVLKIAKERSDLIVLCGGLGPTEDDL   76
NTDB id 1009080 ABKA15 RS00510 WP 049514652.1  ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLASLGVDVYFQTAVGDNKARLLSILEIARNRSNLVILTGGLGPTEDDL   76
NTDB id 170 SP RS09755 WP 000642718.1          ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEVRLLSLLEIASQRSSLVILTGGLGPTEDDL   76
NTDB id 280 KZH43 RS08670 WP 000642700.1       ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEVRLLSLLEIASQRSSLVILTGGLGATEDDL   76
NTDB id 205 SPR RS08830 WP 000642700.1         ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEVRLLSLLEIASQRSSLVILTGGLGATEDDL   76
NTDB id 239 SPD RS09270 WP 000642701.1         ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEVRLLSLLEIASQRSSLVILTGGLGATEDDL   76
NTDB id 538 SMSK321 RS11060 WP 000642686.1     ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEARLLSLLEIASQRSSLVILTGGLGPTEDDL   76
NTDB id 510 SM12261 RS08320 WP 000642690.1     ....MKAEIIAVGTEILTGQIVNTNAQFLSEKLAEIGVDVYFQTAVGDNEARLLSLLEIASQRSSLVILTGGLGPTEDDL   76
consensus                                       *!*!*!!!!*!*!*!!!*!!!*!!*!***!**!**!***!!!!!! !!******!**!!*****!!!!*!*!!!

logo
NTDB id 124 BSU 16930 NP 389575.2              TKETIANTLGRPLVLNDEAFQSIEDYFK.RTKRTMSPNNRKQALVIEGSDVLANHFGMAPGMLTEHESRYYMLLPGPPSE  159
NTDB id 462 GPW51 RS00385 WP 012774894.1       TKQTLATFLGRNLVFDELAMAKLDRFFASRPGRVRTPNNERQAQIVEGSQALQNPAGLAVGGMIEQDGVTYIVLPGPPSE  156
NTDB id 412 SMU RS09535 WP 002262393.1         TKQTLAKFLKRELVFDKTAQERLDEFFASRPTSMRTPNNECQAQITAGSQPLSNKTGLAVGGLLEADGVTYVVLPGPPSE  156
NTDB id 1009080 ABKA15 RS00510 WP 049514652.1  TKQTLSKFLNRRLVFDRMATEKLDRFFASRSDYVRTPNNERQAQIVEGSTPLQNETGLAVGGVIEVSGVTYVVLPGPPSE  156
NTDB id 170 SP RS09755 WP 000642718.1          TKQTLAKFLGKALVFDPQAQEKLDIFFTLRPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE  156
NTDB id 280 KZH43 RS08670 WP 000642700.1       TKQTLAKFLGKALVFDPQAQEKLDIFFALRPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE  156
NTDB id 205 SPR RS08830 WP 000642700.1         TKQTLAKFLGKALVFDPQAQEKLDIFFALRPDYARTPNNERQAQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE  156
NTDB id 239 SPD RS09270 WP 000642701.1         TKQTLAKFLGKALVFDPQAQEKLDIFFALRPDYARTPNNERQVQIVEGAIPLPNETGLAVGGKLEVDGVTYVVLPGPPSE  156
NTDB id 538 SMSK321 RS11060 WP 000642686.1     TKQTLAKFLGKELVFDPQAQEKLDVFFAQRPDYARTPNNERQAQIVEGATPLPNETGLAVGGILEVDGVTYVVLPGPPSE  156
NTDB id 510 SM12261 RS08320 WP 000642690.1     TKQTLAKFLGKELVFDPQAQEKLDVFFAQRPDYARTPNNERQAQLVEGAIPLPNETGLAVGGILEVDGVTYVVLPGPPSE  156
consensus                                      !!*!****!** !!****!*******!* !******!!!**!*****!***!*!**!*!*!***!*****!**!!!!!!!

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NTDB id 124 BSU 16930 NP 389575.2              LRPMFENEAKPLLLKKMGSNEKIVSTVLRFFGIGESQLEADLEDIIDAQTNPTIAPLAADGEVTLRLTAKHADEKETERL  239
NTDB id 462 GPW51 RS00385 WP 012774894.1       LKAMFSESLLPLLSQ...SQQQLYSRVLRFFGIGESQLVTVLADVIDKQTDPTLAPYAKVGEVTLRLSTKATSQEEANLR  233
NTDB id 412 SMU RS09535 WP 002262393.1         LKPMVNKELLPYLSK...TSEKLYSRVLRFFGIGESHLVTLLHDLIAEQTDPTIAPYAKTGEVTIRLSTKAHRQKEADSK  233
NTDB id 1009080 ABKA15 RS00510 WP 049514652.1  LKPMVNNELVPLLA....TGQKLYSRVLRFFGIGESQLVTLLGDLIDNQTDPTIAPYAKTGEVTLRLSTKAGSQKEADVK  232
NTDB id 170 SP RS09755 WP 000642718.1          LKPMVLNQLLPKLM....TGSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA  232
NTDB id 280 KZH43 RS08670 WP 000642700.1       LKPMVLNQLLPKLM....TGSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA  232
NTDB id 205 SPR RS08830 WP 000642700.1         LKPMVLNQLLPKLM....TGSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA  232
NTDB id 239 SPD RS09270 WP 000642701.1         LKPMVLNQLLPKLM....TGSKLYSRVLRFFGIGESQLVTILADLIDNQIDPTLAPYAKTGEVTLRLSTKASSQEEANQA  232
NTDB id 538 SMSK321 RS11060 WP 000642686.1     LKPMVLNQLLPKLM....TGSKLYSRVLRFFGIGESQLVTILSDLIDNQTDPTLAPYAKTGEVTLRLSTKASSQEEANQV  232
NTDB id 510 SM12261 RS08320 WP 000642690.1     LKPMVLNQLLPKLM....TGSKLHSRVLRFFGIGESQLVTILSDLIDNQTDPTLAPYAKTGEVTLRLSTKASSQEEANQV  232
consensus                                      !**!******!*!*    ******!*!!!!!!!!!!!!*!***!*!*!**!**!!*!!*!**!!!!!*!!**!*****!***
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NTDB id 124 BSU 16930 NP 389575.2                LKETEAVILE.......RVGEFFYGYDD.TSLVKELSIACKEKGITISAAESFTGGLFSEWLTDHSGASKLFAGGVVCYT   311
NTDB id 462 GPW51 RS00385 WP 012774894.1         LNQLEEDILQHD.....KLADYFYAYGEDNSLVKTVATRLAEKRQTIAIVEQGTGGLLQAELSLALADQPYFSGGKVVGQ   308
NTDB id 412 SMU RS09535 WP 002262393.1           LDKLEKKITID.....NLADYFYGYGEENSLPQVVFDLLKEKGKTITAAESLTAGLFQARLADFAGASDIFKGGFITYS   308
NTDB id 1009080 ABKA15 RS00510 WP 049514652.1    FAHLEKKILAVQTFEKQHLADLFYAYGDDNSLGQTAFELLRRAGKTVTAAESLTAGLFQATLANFAGASNVFSGGFVTYS   312
NTDB id 170 SP RS09755 WP 000642718.1            LDILENQILDCQTFEGISLRDFCYGYGEETSLASIVVEELKRQGKTIAAAESLTAGLFQATVANFSGVSSIFKGGFVTYS   312
NTDB id 280 KZH43 RS08670 WP 000642700.1         LDILENQILDCQTFEGISLRDFCYGYGEETSLASIVVEELKRQGKTIAAAESLTAGLFQATVANFSGVSSIFEGGFVTYS   312
NTDB id 205 SPR RS08830 WP 000642700.1           LDILENQILDCQTFEGISLRDFCYGYGEETSLASIVVEELKRQGKTIAAAESLTAGLFQATVANFSGVSSIFEGGFVTYS   312
NTDB id 239 SPD RS09270 WP 000642701.1           LDILENQILDCQTFEGISLRDFCYGYGEETSLASIVVEELKRQGKTIAAAESLTAGLFQATVANFSGVSSIFEGGFVTYS   312
NTDB id 538 SMSK321 RS11060 WP 000642686.1       LDILENQILGRQTFEGLSLRDLCYGYGEEASLASIVVEELKKQGKTITAAESLTAGLFQATVADFSGASSIFKGGFVTYS   312
NTDB id 510 SM12261 RS08320 WP 000642690.1       LDILENQILGRQTFEGLSLRDLCYGYGEETSLASIVVEELKRQGKTITSAESLTAGLFQARVADFSGASSIFKGGFVTYS   312
consensus                                        ****!**!** ************!*!****!!**************!****!**!*!!***************!  !!*****

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NTDB id 124 BSU 16930 NP 389575.2                NDVKQNVLGVKKETLDRFGAVSKECASELAKGVQKLTGSDIGISFTGVAGPDAQEGHEPGHVFIGISANGKEEVHEFHFA   391
NTDB id 462 GPW51 RS00385 WP 012774894.1         LGI.................ESGWLSE.EADCIRQELQADLGLAVSVLIKPESTEDNVLAKVYLTLATPSGISQKEIDLG   370
NTDB id 412 SMU RS09535 WP 002262393.1           IEEKARMLGIPFEDLQLHGVVSAFTAEKMAERSRQLTQADLAISLTGVAGPDSLEGQPAGTVFIGLSSSKRTMAIKVLIG   388
NTDB id 1009080 ABKA15 RS00510 WP 049514652.1    IEEKSRMLGISLADLGKHGVVSAFTAEKMAEQARKLTASDYAVSLTGVAGPDSLEGHPAGTVYIGLATTEDVQSIKVNIA   392
NTDB id 170 SP RS09755 WP 000642718.1            LEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGTEVIKVNIG   392
NTDB id 280 KZH43 RS08670 WP 000642700.1         LEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGTEVIKVNIG   392
NTDB id 205 SPR RS08830 WP 000642700.1           LEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGTEVIKVNIG   392
NTDB id 239 SPD RS09270 WP 000642701.1           LEEKSRMLDIPAKNLEEHGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPVGTVFIGLAQDQGTEVIKVNIG   392
NTDB id 538 SMSK321 RS11060 WP 000642686.1       LEEKSKMLDIPVKDLEEQGVVSEFTAQKMAEQARSKTQSDFGISLTGVAGPDSLEGHPAGTVFIGLAQEHGTKVIKVNIG   392
NTDB id 510 SM12261 RS08320 WP 000642690.1       LEEKSKMLDIPVKDLEEQGVVSEFTAQKMAEQARTKTQSDFGLSLTGVAGPDSLEGHPAGTVFIGLAQEQGTEVIKVNIG   392
consensus                                        *********** * *******!*******!*********!**********!***!******!*******************

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NTDB id 124 BSU 16930 NP 389575.2                GSR.TGIRKRGAKYGCHLILKLLEQK....   416
NTDB id 462 GPW51 RS00385 WP 012774894.1         GYSWQYLRQLACLQAWDFVRNTL.......   393
NTDB id 412 SMU RS09535 WP 002262393.1           GRSRSDVRYIAVLHAFNLVRQTLLSHKNLV   418
NTDB id 1009080 ABKA15 RS00510 WP 049514652.1    GRSRTDVRKIAVLHAFNLLRKTLLKNENML   422
NTDB id 170 SP RS09755 WP 000642718.1            GRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 280 KZH43 RS08670 WP 000642700.1         GRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 205 SPR RS08830 WP 000642700.1           GRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 239 SPD RS09270 WP 000642701.1           GRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 538 SMSK321 RS11060 WP 000642686.1       GRSRADVRHIAVMHAFNLVRKALLSD....   418
NTDB id 510 SM12261 RS08320 WP 000642690.1       GRSRADVRHIAVMHAFNLVRKALLSD....   418
consensus                                        !******!**************!***
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X non conserved

X similar

X ≥ 50% conserved